

## SEQUENCE LISTING

<110> Novozymes A/S  
<120> Detection system for high expressing recombinant Bacillus  
<130> 10355  
<160> 11  
<170> PatentIn version 3.2

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<212> DNA  
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<222> (1000)..(2349)  
<223> 1-999 is promoter

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taaatagaca tgtgaaaata gagaaacgga gtgaacatg atg gat aac tat cgt	1014		
Met Asp Asn Tyr Arg			
1	5		
gat gaa aac aga acg aaa ggt aat gag aat gag gtc ttt tta acg aaa	1062		
Asp Glu Asn Arg Thr Lys Gly Asn Glu Asn Glu Val Phe Leu Thr Lys			
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gag aac gat cag agc gcc tcc tac tcg gcc cgc aat gtc att cat gat	1110		
Glu Asn Asp Gln Ser Ala Ser Tyr Ser Ala Arg Asn Val Ile His Asp			
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cag gag aag aaa aaa cga gga ttc gga tgg ttc aga ccg ttg ctt ggc	1158		
Gln Glu Lys Lys Arg Gly Phe Gly Trp Phe Arg Pro Leu Leu Gly			
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gga gtg atc ggc ggc agt ctt gct ctt ggc att tac acg ttt aca ccg	1206		
Gly Val Ile Gly Gly Ser Leu Ala Leu Gly Ile Tyr Thr Phe Thr Pro			
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ctt ggt aac cat gat tct cag gac act gca aaa caa tca tcc agc cag	1254		
Leu Gly Asn His Asp Ser Gln Asp Thr Ala Lys Gln Ser Ser Ser Gln			
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cag caa acg caa tct gtt aca gca aca agc acc tcc tct gaa tct aaa	1302		
Gln Gln Thr Gln Ser Val Thr Ala Thr Ser Thr Ser Ser Glu Ser Lys			
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aaa agc tca agc agc tca tct gca ttc aag agc gag gac tct tct aaa	1350		
Lys Ser Ser Ser Ser Ser Ala Phe Lys Ser Glu Asp Ser Ser Lys			
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atc tca gat atg gta gaa gac ctt tca cca gcg att gtc ggt att aca	1398		
Ile Ser Asp Met Val Glu Asp Leu Ser Pro Ala Ile Val Gly Ile Thr			
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aat ctt cag gca caa tca aac agc tct ttg ttc ggc tct agt tct tct	1446		
Asn Leu Gln Ala Gln Ser Asn Ser Leu Phe Gly Ser Ser Ser Ser			
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gat tcc agc gaa gat aca gaa agc ggt tca ggg tca ggt gtc att ttc	1494		
Asp Ser Ser Glu Asp Thr Glu Ser Gly Ser Gly Val Ile Phe			
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aaa aaa gag aat ggc aag gct tat atc att aca aat aac cac gtc gta	1542		
Lys Lys Glu Asn Gly Lys Ala Tyr Ile Ile Thr Asn Asn His Val Val			
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gaa ggg gca tca tca ctg aag gta tct tta tat gac ggc act gag gtt	1590		
Glu Gly Ala Ser Ser Leu Lys Val Ser Leu Tyr Asp Gly Thr Glu Val			
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act gca aag ctg gta ggc agt gac tcg tta act gat tta gcc gtc ctc	1638		
Thr Ala Lys Leu Val Gly Ser Asp Ser Leu Thr Asp Leu Ala Val Leu			
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caa atc agt gat gac cac gtc aca aaa gtg gca aac ttc ggt gat tca	1686		
Gln Ile Ser Asp Asp His Val Thr Lys Val Ala Asn Phe Gly Asp Ser			

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tct gat ctt aga aca ggc gag acc gtt att gcg att ggg gat ccg ctt Ser Asp Leu Arg Thr Gly Glu Thr Val Ile Ala Ile Gly Asp Pro Leu	230	235	1734
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gga aaa gac ctg tcc cgc aca gta aca caa gga att gta agc ggc gtg Gly Lys Asp Leu Ser Arg Thr Val Thr Gln Gly Ile Val Ser Gly Val	250	255	1782
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gac aga acg gtt tca atg tct aca tca gcc ggc gaa acg agc att aac Asp Arg Thr Val Ser Met Ser Thr Ser Ala Gly Glu Thr Ser Ile Asn	265	270	1830
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gtc att cag aca gac gca gca att aat cca ggt aac agc ggc ggt cct Val Ile Gln Thr Asp Ala Ala Ile Asn Pro Gly Asn Ser Gly Gly Pro	280	285	1878
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ttg tta aat aca gac ggc aaa att gtc ggc att aac agt atg aaa atc Leu Leu Asn Thr Asp Gly Lys Ile Val Gly Ile Asn Ser Met Lys Ile	295	300	1926
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agt gag gat gat gtt gag ggt atc gga ttc gcc att cca agc aat gac Ser Glu Asp Asp Val Glu Gly Ile Gly Phe Ala Ile Pro Ser Asn Asp	310	315	1974
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gta aaa ccg att got gaa gaa ttg ctg tct aaa gga caa att gaa cgt Val Lys Pro Ile Ala Glu Glu Leu Leu Ser Lys Gly Gln Ile Glu Arg	330	335	2022
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cca tat atc ggt gtc agc atg ctt gat cta gag caa gtg ccg caa aat Pro Tyr Ile Gly Val Ser Met Leu Asp Leu Glu Gln Val Pro Gln Asn	345	350	2070
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tac caa gaa ggc aca ctc ggc ctg ttc ggc agc cag ctg aat aaa ggc Tyr Gln Glu Gly Thr Leu Gly Leu Phe Gly Ser Gln Leu Asn Lys Gly	360	365	2118
370			
gtt tac atc cgt gag gtc gct tca ggc tct cct gct gaa aag gcc gga Val Tyr Ile Arg Glu Val Ala Ser Gly Ser Pro Ala Glu Lys Ala Gly	375	380	2166
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aca ggc agt gaa ttg cgc aat atc tta tat aaa gac gca aag atc ggt Thr Gly Ser Glu Leu Arg Asn Ile Leu Tyr Lys Asp Ala Lys Ile Gly	410	415	2262
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gat acc gtt gaa gtg aaa att ctc cga aac ggc aaa gaa atg acg aaa Asp Thr Val Glu Val Lys Ile Leu Arg Asn Gly Lys Glu Met Thr Lys	425	430	2310
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Arg Pro Leu Leu Gly Gly Val Ile Gly Gly Ser Leu Ala Leu Gly Ile  
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Tyr Thr Phe Thr Pro Leu Gly Asn His Asp Ser Gln Asp Thr Ala Lys  
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Gln Ser Ser Ser Gln Gln Thr Gln Ser Val Thr Ala Thr Ser Thr  
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Ser Gly Val Ile Phe Lys Lys Glu Asn Gly Lys Ala Tyr Ile Ile Thr  
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Ile Val Ser Gly Val Asp Arg Thr Val Ser Met Ser Thr Ser Ala Gly  
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Glu Thr Ser Ile Asn Val Ile Gln Thr Asp Ala Ala Ile Asn Pro Gly  
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Asn Ser Gly Gly Pro Leu Leu Asn Thr Asp Gly Lys Ile Val Gly Ile  
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Asn Ser Met Lys Ile Ser Glu Asp Asp Val Glu Gly Ile Gly Phe Ala  
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Ile Pro Ser Asn Asp Val Lys Pro Ile Ala Glu Glu Leu Leu Ser Lys  
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Gly Gln Ile Glu Arg Pro Tyr Ile Gly Val Ser Met Leu Asp Leu Glu  
340 345 350

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Gln Leu Asn Lys Gly Val Tyr Ile Arg Glu Val Ala Ser Gly Ser Pro  
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Ala Glu Lys Ala Gly Leu Lys Ala Glu Asp Ile Ile Ile Gly Leu Lys  
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Gly Lys Glu Ile Asp Thr Gly Ser Glu Leu Arg Asn Ile Leu Tyr Lys  
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26